GenCore version 5.1.9


OM nucleic - nucleic search, using sw model

Run on: August 9, 2006, 21:57:27 ; Search time 9811 Seconds
(without alignments)
10989.232 Million cell updates/sec

Title: US-08-906-365-1
Perfect score: 1686
Sequence: 1 cagccattatacttgcccac.....agaacccacagtctcagtga 1686

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 6366136 seqs, 31973710525 residues

Total number of hits satisfying chosen parameters: 12732272

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : GenEmbl:*
1: gb_env:*
2: gb_pat:*
3: gb_ph:*
4: gb_pl:*
5: gb_pr:*
6: gb_ro:*
7: gb_sts:*
8: gb_sy:*
9: gb_un:*
10: gb_vi:*
11: gb_ov:*
12: gb_htg:*
13: gb_in:*
14: gb_om:*
15: gb_ba:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | % Query Match | Length | DB | ID | Description |
|---|---|---|---|---|---|---|
| 1 | 1684.4 | 99.9 | 1740 | 2 | BD093391 | BD093391 Method fo |
| 2 | 1684.4 | 99.9 | 1740 | 5 | AB006590 | AB006590 Homo sapi |
| 3 | 1683.4 | 99.8 | 2011 | 2 | AR606192 | AR606192 Sequence |
| 4 | 1683.4 | 99.8 | 2011 | 2 | AX234658 | AX234658 Sequence |
| 5 | 1683.4 | 99.8 | 2011 | 2 | AX676912 | AX676912 Sequence |
| 6 | 1683.4 | 99.8 | 2011 | 5 | AF051427 | AF051427 Homo sapi |
| 7 | 1667.4 | 98.9 | 1898 | 2 | A65127 | A65127 Sequence 24 |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| | 8 | 1667.4 | 98.9 | 1898 | 2 | AR454163 | AR454163 Sequence |
| | 9 | 1667.4 | 98.9 | 1898 | 2 | AR490594 | AR490594 Sequence |
| | 10 | 1667.4 | 98.9 | 1898 | 2 | AX323078 | AX323078 Sequence |
| | 11 | 1637.4 | 97.1 | 2433 | 2 | BD170497 | BD170497 Fluoresce |
| | 12 | 1634 | 96.9 | 1647 | 2 | BD091391 | BD091391 Estrogen |
| | 13 | 1634 | 96.9 | 1647 | 2 | AR233984 | AR233984 Sequence |
| | 14 | 1634 | 96.9 | 1647 | 2 | AR316860 | AR316860 Sequence |
| | 15 | 1634 | 96.9 | 1647 | 2 | AX029400 | AX029400 Sequence |
| | 16 | 1609.4 | 95.5 | 1660 | 2 | AX592833 | AX592833 Sequence |
| c | 17 | 1609.4 | 95.5 | 1660 | 2 | AX592834 | AX592834 Sequence |
| | 18 | 1496.4 | 88.8 | 2041 | 5 | AF051428 | AF051428 Homo sapi |
| | 19 | 1496.4 | 88.8 | 2745 | 5 | AF060555 | AF060555 Homo sapi |
| | 20 | 1495.8 | 88.7 | 3593 | 5 | AB006589 | AB006589 Homo sapi |
| | 21 | 1485.6 | 88.1 | 1651 | 5 | CJERB | Y09372 C.jacchus m |
| | 22 | 1453.6 | 86.2 | 1460 | 2 | A61586 | A61586 Sequence 4 |
| | 23 | 1453.6 | 86.2 | 1460 | 2 | AR075921 | AR075921 Sequence |
| | 24 | 1453.6 | 86.2 | 1460 | 2 | BD131061 | BD131061 Orphan re |
| | 25 | 1453.6 | 86.2 | 1460 | 2 | AX022458 | AX022458 Sequence |
| | 26 | 1450.4 | 86.0 | 1460 | 2 | BD078109 | BD078109 Discrimin |
| | 27 | 1450 | 86.0 | 1560 | 5 | HSRNAERB | X99101 H.sapiens m |
| | 28 | 1434 | 85.1 | 1434 | 2 | A65104 | A65104 Sequence 1 |
| | 29 | 1434 | 85.1 | 1434 | 2 | AR454145 | AR454145 Sequence |
| | 30 | 1434 | 85.1 | 1434 | 2 | AR490576 | AR490576 Sequence |
| | 31 | 1434 | 85.1 | 1434 | 2 | AX323055 | AX323055 Sequence |
| | 32 | 1405.2 | 83.3 | 5554 | 5 | AB209620 | AB209620 Homo sapi |
| | 33 | 1374.2 | 81.5 | 1640 | 5 | AF393815 | AF393815 Macaca ar |
| | 34 | 1306.6 | 77.5 | 1566 | 5 | AF393816 | AF393816 Callithri |
| | 35 | 1256.6 | 74.5 | 1611 | 14 | AF110402 | AF110402 Bos tauru |
| | 36 | 1254.6 | 74.4 | 1584 | 14 | AF177936 | AF177936 Ovis arie |
| | 37 | 1247.2 | 74.0 | 2344 | 6 | AB190769 | AB190769 Rattus no |
| | 38 | 1247 | 74.0 | 1251 | 2 | A65105 | A65105 Sequence 2 |
| | 39 | 1247 | 74.0 | 1251 | 2 | AR454146 | AR454146 Sequence |
| | 40 | 1247 | 74.0 | 1251 | 2 | AR490577 | AR490577 Sequence |
| | 41 | 1247 | 74.0 | 1251 | 2 | AX323056 | AX323056 Sequence |
| | 42 | 1247 | 74.0 | 1257 | 2 | A65123 | A65123 Sequence 20 |
| | 43 | 1247 | 74.0 | 1257 | 2 | AR454160 | AR454160 Sequence |
| | 44 | 1247 | 74.0 | 1257 | 2 | AR490591 | AR490591 Sequence |
| | 45 | 1247 | 74.0 | 1257 | 2 | AX323074 | AX323074 Sequence |

GenCore version 5.1.9


OM nucleic - nucleic search, using sw model

Run on: August 10, 2006, 00:28:57 ; Search time 341 Seconds
(without alignments)
9251.289 Million cell updates/sec

Title: US-08-906-365-1
Perfect score: 1686
Sequence: 1 cagccattatacttgcccac.....agaacccacagtctcagtga 1686

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1403666 seqs, 935554401 residues

Total number of hits satisfying chosen parameters: 2807332

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_NA:*
1: /EMC_Celerra_SIDS3/ptodata/2/ina/1_COMB.seq:*
2: /EMC_Celerra_SIDS3/ptodata/2/ina/5_COMB.seq:*
3: /EMC_Celerra_SIDS3/ptodata/2/ina/6A_COMB.seq:*
4: /EMC_Celerra_SIDS3/ptodata/2/ina/6B_COMB.seq:*
5: /EMC_Celerra_SIDS3/ptodata/2/ina/7_COMB.seq:*
6: /EMC_Celerra_SIDS3/ptodata/2/ina/H_COMB.seq:*
7: /EMC_Celerra_SIDS3/ptodata/2/ina/PCTUS_COMB.seq:*
8: /EMC_Celerra_SIDS3/ptodata/2/ina/PP_COMB.seq:*
9: /EMC_Celerra_SIDS3/ptodata/2/ina/RE_COMB.seq:*
10: /EMC_Celerra_SIDS3/ptodata/2/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | % Query Match | Length | DB | ID | Description |
|---|---|---|---|---|---|---|
| 1 | 1684.4 | 99.9 | 1745 | 3 | US-09-949-016-1563 | Sequence 1563, Ap |
| 2 | 1683.4 | 99.8 | 2011 | 3 | US-09-768-185A-2 | Sequence 2, Appli |
| 3 | 1667.4 | 98.9 | 1898 | 3 | US-09-608-088-24 | Sequence 24, Appl |
| 4 | 1667.4 | 98.9 | 1898 | 3 | US-09-711-288-24 | Sequence 24, Appl |
| 5 | 1634 | 96.9 | 1647 | 3 | US-09-139-617-2 | Sequence 2, Appli |
| 6 | 1634 | 96.9 | 1647 | 3 | US-09-561-741A-2 | Sequence 2, Appli |
| 7 | 1634 | 96.9 | 1647 | 3 | US-09-558-795-2 | Sequence 2, Appli |
| 8 | 1453.6 | 86.2 | 1460 | 2 | US-08-836-620A-4 | Sequence 4, Appli |
| 9 | 1434 | 85.1 | 1434 | 3 | US-09-608-088-1 | Sequence 1, Appli |
| 10 | 1434 | 85.1 | 1434 | 3 | US-09-711-288-1 | Sequence 1, Appli |
| 11 | 1247 | 74.0 | 1251 | 3 | US-09-608-088-2 | Sequence 2, Appli |
| 12 | 1247 | 74.0 | 1251 | 3 | US-09-711-288-2 | Sequence 2, Appli |

| | | | | | | |
|---|---|---|---|---|---|---|
| 13 | 1247 | 74.0 | 1257 | 3 | US-09-608-088-20 | Sequence 20, Appl |
| 14 | 1247 | 74.0 | 1257 | 3 | US-09-711-288-20 | Sequence 20, Appl |
| 15 | 1233.6 | 73.2 | 2568 | 2 | US-08-836-620A-1 | Sequence 1, Appli |
| 16 | 1099.6 | 65.2 | 1458 | 2 | US-08-836-620A-6 | Sequence 6, Appli |
| 17 | 453.4 | 26.9 | 68452 | 3 | US-09-949-016-13305 | Sequence 13305, A |
| 18 | 453.4 | 26.9 | 325791 | 3 | US-09-768-185A-1 | Sequence 1, Appli |
| 19 | 395.8 | 23.5 | 2764 | 3 | US-09-893-666A-1 | Sequence 1, Appli |
| 20 | 390.8 | 23.2 | 4963 | 2 | US-08-076-726-16 | Sequence 16, Appl |
| 21 | 390.8 | 23.2 | 4963 | 2 | US-08-260-452-9 | Sequence 9, Appli |
| 22 | 390.8 | 23.2 | 4963 | 2 | US-08-481-970-9 | Sequence 9, Appli |
| 23 | 390.8 | 23.2 | 4963 | 2 | US-08-897-719-9 | Sequence 9, Appli |
| 24 | 390.8 | 23.2 | 4963 | 3 | US-09-163-269-9 | Sequence 9, Appli |
| 25 | 390.8 | 23.2 | 4963 | 3 | US-09-281-674-9 | Sequence 9, Appli |
| 26 | 390.8 | 23.2 | 4963 | 3 | US-09-777-317B-9 | Sequence 9, Appli |
| 27 | 389.2 | 23.1 | 2092 | 3 | US-10-052-092-6 | Sequence 6, Appli |
| 28 | 389.2 | 23.1 | 6450 | 3 | US-09-041-886-34 | Sequence 34, Appl |
| 29 | 389.2 | 23.1 | 6450 | 3 | US-08-453-998-1 | Sequence 1, Appli |
| 30 | 389.2 | 23.1 | 6450 | 3 | US-10-027-983-3 | Sequence 3, Appli |
| 31 | 389.2 | 23.1 | 6450 | 3 | US-09-949-016-18 | Sequence 18, Appl |
| 32 | 389.2 | 23.1 | 6450 | 3 | US-10-052-092-1 | Sequence 1, Appli |
| 33 | 389.2 | 23.1 | 6450 | 3 | US-10-052-092-7 | Sequence 7, Appli |
| 34 | 389.2 | 23.1 | 6450 | 3 | US-10-081-563-1 | Sequence 1, Appli |
| 35 | 389.2 | 23.1 | 6610 | 3 | US-10-052-092-20 | Sequence 20, Appl |
| 36 | 388 | 23.0 | 1788 | 3 | US-10-052-092-24 | Sequence 24, Appl |
| 37 | 366.2 | 21.7 | 1978 | 3 | US-10-052-092-23 | Sequence 23, Appl |
| 38 | 326.6 | 19.4 | 2106 | 3 | US-10-052-092-5 | Sequence 5, Appli |
| 39 | 312.4 | 18.5 | 8566 | 3 | US-10-027-983-10 | Sequence 10, Appl |
| 40 | 296.4 | 17.6 | 2495 | 3 | US-09-771-357-104 | Sequence 104, App |
| 41 | 296.4 | 17.6 | 2495 | 3 | US-10-059-579A-104 | Sequence 104, App |
| 42 | 287.2 | 17.0 | 1218 | 3 | US-10-027-983-98 | Sequence 98, Appl |
| 43 | 285.6 | 16.9 | 1644 | 3 | US-10-052-092-2 | Sequence 2, Appli |
| 44 | 285.6 | 16.9 | 1956 | 3 | US-08-693-940-2 | Sequence 2, Appli |
| 45 | 285.6 | 16.9 | 1956 | 3 | US-09-566-660-2 | Sequence 2, Appli |

GenCore version 5.1.9


OM nucleic - nucleic search, using sw model

Run on: August 10, 2006, 00:59:46 ; Search time 2247 Seconds
(without alignments)
9219.828 Million cell updates/sec

Title: US-08-906-365-1
Perfect score: 1686
Sequence: 1 cagccattatacttgcccac.....agaacccacagtctcagtga 1686

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 18892170 seqs, 6143817638 residues

Total number of hits satisfying chosen parameters: 37784340

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published_Applications_NA_Main:*
1: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US07_PUBCOMB.seq:*
2: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US08_PUBCOMB.seq:*
3: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US09A_PUBCOMB.seq:*
4: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US09B_PUBCOMB.seq:*
5: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US09C_PUBCOMB.seq:*
6: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10A_PUBCOMB.seq:*
7: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10B_PUBCOMB.seq:*
8: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10C_PUBCOMB.seq:*
9: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10D_PUBCOMB.seq:*
10: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10E_PUBCOMB.seq:*
11: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10F_PUBCOMB.seq:*
12: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10G_PUBCOMB.seq:*
13: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11A_PUBCOMB.seq:*
14: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11B_PUBCOMB.seq:*
15: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11C_PUBCOMB.seq:*
16: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11D_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | % Query Match | Length | DB | ID | Description |
|---|---|---|---|---|---|---|
| 1 | 1686 | 100.0 | 1686 | 9 | US-10-745-379-1 | Sequence 1, Appli |
| 2 | 1686 | 100.0 | 1686 | 16 | US-11-026-800-1 | Sequence 1, Appli |
| 3 | 1684.4 | 99.9 | 1740 | 3 | US-09-815-068A-1 | Sequence 1, Appli |
| 4 | 1684.4 | 99.9 | 1740 | 6 | US-10-198-785-1 | Sequence 1, Appli |
| 5 | 1683.4 | 99.8 | 2011 | 4 | US-09-768-185A-2 | Sequence 2, Appli |
| 6 | 1683.4 | 99.8 | 2011 | 6 | US-10-157-031-105 | Sequence 105, App |

| | | | | | | |
|---|---|---|---|---|---|---|
| 7 | 1683.4 | 99.8 | 2011 | 7 | US-10-392-274-3 | Sequence 3, Appli |
| 8 | 1683.4 | 99.8 | 2011 | 10 | US-10-888-313A-101 | Sequence 101, App |
| 9 | 1683.4 | 99.8 | 6777 | 7 | US-10-376-566-10 | Sequence 10, Appl |
| 10 | 1637.4 | 97.1 | 2433 | 8 | US-10-460-845-1 | Sequence 1, Appli |
| 11 | 1496.4 | 88.8 | 2041 | 10 | US-10-756-149-1507 | Sequence 1507, Ap |
| 12 | 1496.4 | 88.8 | 2745 | 11 | US-10-826-585-22 | Sequence 22, Appl |
| 13 | 1495.8 | 88.7 | 3593 | 7 | US-10-376-566-3 | Sequence 3, Appli |
| 14 | 1453.6 | 86.2 | 1460 | 6 | US-10-278-481-4 | Sequence 4, Appli |
| 15 | 1433.8 | 85.0 | 1682 | 7 | US-10-373-271-2 | Sequence 2, Appli |
| 16 | 1236.4 | 73.3 | 2555 | 16 | US-11-136-527-2114 | Sequence 2114, Ap |
| 17 | 1233.6 | 73.2 | 2568 | 6 | US-10-278-481-1 | Sequence 1, Appli |
| 18 | 1167.4 | 69.2 | 1427 | 7 | US-10-376-566-15 | Sequence 15, Appl |
| 19 | 1099.6 | 65.2 | 1458 | 6 | US-10-278-481-6 | Sequence 6, Appli |
| 20 | 1056.4 | 62.7 | 1512 | 16 | US-11-136-527-3577 | Sequence 3577, Ap |
| 21 | 865 | 51.3 | 1215 | 7 | US-10-376-566-14 | Sequence 14, Appl |
| 22 | 600 | 35.6 | 600 | 13 | US-11-060-756-2172 | Sequence 2172, Ap |
| 23 | 600 | 35.6 | 600 | 13 | US-11-060-756-2173 | Sequence 2173, Ap |
| 24 | 600 | 35.6 | 600 | 13 | US-11-060-756-6444 | Sequence 6444, Ap |
| 25 | 600 | 35.6 | 600 | 13 | US-11-060-756-6445 | Sequence 6445, Ap |
| 26 | 453.4 | 26.9 | 113000 | 7 | US-10-376-566-16 | Sequence 16, Appl |
| 27 | 453.4 | 26.9 | 325791 | 4 | US-09-768-185A-1 | Sequence 1, Appli |
| 28 | 452.4 | 26.8 | 597 | 3 | US-09-864-761-7903 | Sequence 7903, Ap |
| 29 | 433.8 | 25.7 | 2384 | 8 | US-10-663-561-148 | Sequence 148, App |
| 30 | 415.8 | 24.7 | 2188 | 8 | US-10-663-561-147 | Sequence 147, App |
| 31 | 396.8 | 23.5 | 600 | 16 | US-11-136-527-7673 | Sequence 7673, Ap |
| 32 | 395.8 | 23.5 | 2764 | 3 | US-09-893-666A-1 | Sequence 1, Appli |
| 33 | 391.2 | 23.2 | 2043 | 8 | US-10-663-561-146 | Sequence 146, App |
| 34 | 390.8 | 23.2 | 1788 | 3 | US-09-853-033-1 | Sequence 1, Appli |
| 35 | 390.8 | 23.2 | 4963 | 3 | US-09-281-674-9 | Sequence 9, Appli |
| 36 | 390.8 | 23.2 | 4963 | 3 | US-09-777-317-9 | Sequence 9, Appli |
| 37 | 390.8 | 23.2 | 4963 | 3 | US-09-892-227-9 | Sequence 9, Appli |
| 38 | 389.2 | 23.1 | 1785 | 7 | US-10-095-373A-1 | Sequence 1, Appli |
| 39 | 389.2 | 23.1 | 1793 | 13 | US-11-035-623-1 | Sequence 1, Appli |
| 40 | 389.2 | 23.1 | 1809 | 13 | US-11-035-623-11 | Sequence 11, Appl |
| 41 | 389.2 | 23.1 | 2092 | 3 | US-09-952-680A-9 | Sequence 9, Appli |
| 42 | 389.2 | 23.1 | 2092 | 6 | US-10-052-092-6 | Sequence 6, Appli |
| 43 | 389.2 | 23.1 | 2092 | 7 | US-10-157-899A-54 | Sequence 54, Appl |
| 44 | 389.2 | 23.1 | 2092 | 7 | US-10-437-107-6 | Sequence 6, Appli |
| 45 | 389.2 | 23.1 | 2092 | 9 | US-10-215-982-9 | Sequence 9, Appli |

GenCore version 5.1.9


OM nucleic - nucleic search, using sw model

Run on: August 10, 2006, 03:22:02 ; Search time 563 Seconds
(without alignments)
4755.765 Million cell updates/sec

Title: US-08-906-365-1
Perfect score: 1686
Sequence: 1 cagccattatacttgcccac.....agaacccacagtctcagtga 1686

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 2200221 seqs, 794037843 residues

Total number of hits satisfying chosen parameters: 4400442

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published_Applications_NA_New:*
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2: /EMC_Celerra_SIDS3/ptodata/1/pubpna/US06_NEW_PUB.seq:*
3: /EMC_Celerra_SIDS3/ptodata/1/pubpna/US07_NEW_PUB.seq:*
4: /EMC_Celerra_SIDS3/ptodata/1/pubpna/US08_NEW_PUB.seq:*
5: /EMC_Celerra_SIDS3/ptodata/1/pubpna/PCT_NEW_PUB.seq:*
6: /EMC_Celerra_SIDS3/ptodata/1/pubpna/US10_NEW_PUB.seq:*
7: /EMC_Celerra_SIDS3/ptodata/1/pubpna/US11_NEW_PUB.seq:*
8: /EMC_Celerra_SIDS3/ptodata/1/pubpna/US11_NEW_PUB.seq1:*
9: /EMC_Celerra_SIDS3/ptodata/1/pubpna/US11_NEW_PUB.seq2:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | % Query Match | Length | DB | ID | Description |
|---|---|---|---|---|---|---|
| 1 | 1683.4 | 99.8 | 2011 | 8 | US-11-283-329-93 | Sequence 93, Appl |
| 2 | 1683.4 | 99.8 | 2011 | 9 | US-11-346-759-101 | Sequence 101, App |
| 3 | 1000 | 59.3 | 1000 | 8 | US-11-266-748A-395231 | Sequence 395231, |
| c 4 | 1000 | 59.3 | 1000 | 8 | US-11-266-748A-466277 | Sequence 466277, |
| 5 | 450.4 | 26.7 | 2186 | 6 | US-10-501-227-24 | Sequence 24, Appl |
| 6 | 389.8 | 23.1 | 1824 | 6 | US-10-501-227-5 | Sequence 5, Appli |
| 7 | 389.8 | 23.1 | 3499 | 6 | US-10-501-227-2 | Sequence 2, Appli |
| 8 | 389.2 | 23.1 | 6450 | 8 | US-11-289-102-120 | Sequence 120, App |
| 9 | 389.2 | 23.1 | 6450 | 8 | US-11-283-329-91 | Sequence 91, Appl |
| 10 | 389.2 | 23.1 | 6450 | 9 | US-11-346-759-100 | Sequence 100, App |
| 11 | 352.8 | 20.9 | 963 | 6 | US-10-501-227-25 | Sequence 25, Appl |
| 12 | 319.2 | 18.9 | 996 | 6 | US-10-501-227-3 | Sequence 3, Appli |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| | 13 | 179.6 | 10.7 | 611 | 8 | US-11-266-748A-214650 | Sequence 214650, |
| c | 14 | 130 | 7.7 | 3540 | 8 | US-11-266-748A-71864 | Sequence 71864, A |
| c | 15 | 130 | 7.7 | 3540 | 8 | US-11-266-748A-106889 | Sequence 106889, |
| | 16 | 130 | 7.7 | 3540 | 8 | US-11-266-748A-124675 | Sequence 124675, |
| | 17 | 129 | 7.7 | 1566 | 6 | US-10-526-940-2 | Sequence 2, Appli |
| | 18 | 129 | 7.7 | 2221 | 8 | US-11-283-329-95 | Sequence 95, Appl |
| | 19 | 129 | 7.7 | 2402 | 8 | US-11-266-748A-32133 | Sequence 32133, A |
| | 20 | 113.8 | 6.7 | 1377 | 6 | US-10-526-940-1 | Sequence 1, Appli |
| | 21 | 113.8 | 6.7 | 5216 | 6 | US-10-507-700-5 | Sequence 5, Appli |
| | 22 | 113.8 | 6.7 | 5253 | 8 | US-11-283-329-99 | Sequence 99, Appl |
| | 23 | 112.2 | 6.7 | 1503 | 6 | US-10-526-940-7 | Sequence 7, Appli |
| | 24 | 110.6 | 6.6 | 2193 | 8 | US-11-283-329-97 | Sequence 97, Appl |
| | 25 | 105.8 | 6.3 | 5221 | 6 | US-10-507-700-3 | Sequence 3, Appli |
| | 26 | 95.2 | 5.6 | 3514 | 6 | US-10-523-899-4 | Sequence 4, Appli |
| | 27 | 95.2 | 5.6 | 3768 | 6 | US-10-523-899-1 | Sequence 1, Appli |
| | 28 | 95.2 | 5.6 | 4314 | 8 | US-11-283-329-107 | Sequence 107, App |
| | 29 | 89.6 | 5.3 | 2575 | 9 | US-11-207-382-11 | Sequence 11, Appl |
| | 30 | 88.6 | 5.3 | 2263 | 8 | US-11-266-748A-185290 | Sequence 185290, |
| | 31 | 88.6 | 5.3 | 2263 | 8 | US-11-266-748A-192812 | Sequence 192812, |
| | 32 | 88.6 | 5.3 | 2481 | 8 | US-11-266-748A-59173 | Sequence 59173, A |
| | 33 | 88.6 | 5.3 | 2549 | 8 | US-11-283-329-111 | Sequence 111, App |
| | 34 | 88.6 | 5.3 | 2699 | 8 | US-11-283-329-109 | Sequence 109, App |
| c | 35 | 88.4 | 5.2 | 1442 | 8 | US-11-266-748A-227525 | Sequence 227525, |
| | 36 | 88.4 | 5.2 | 1442 | 8 | US-11-266-748A-241597 | Sequence 241597, |
| | 37 | 88.2 | 5.2 | 1855 | 8 | US-11-266-748A-27269 | Sequence 27269, A |
| | 38 | 88.2 | 5.2 | 2202 | 8 | US-11-283-329-75 | Sequence 75, Appl |
| | 39 | 88 | 5.2 | 1000 | 8 | US-11-266-748A-391580 | Sequence 391580, |
| c | 40 | 88 | 5.2 | 1000 | 8 | US-11-266-748A-482298 | Sequence 482298, |
| c | 41 | 86.4 | 5.1 | 788 | 8 | US-11-266-748A-255985 | Sequence 255985, |
| | 42 | 86.4 | 5.1 | 788 | 8 | US-11-266-748A-316502 | Sequence 316502, |
| | 43 | 86.4 | 5.1 | 3791 | 8 | US-11-266-748A-32110 | Sequence 32110, A |
| | 44 | 86.4 | 5.1 | 3791 | 9 | US-11-207-382-26 | Sequence 26, Appl |
| | 45 | 86.4 | 5.1 | 4788 | 8 | US-11-283-329-101 | Sequence 101, App |

GenCore version 5.1.9


OM nucleic - nucleic search, using sw model

Run on: August 9, 2006, 22:16:02 ; Search time 8466 Seconds
(without alignments)
11136.309 Million cell updates/sec

Title: US-08-906-365-1
Perfect score: 1686
Sequence: 1 cagccattatacttgcccac.....agaacccacagtctcagtga 1686

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 48236798 seqs, 27959665780 residues

Total number of hits satisfying chosen parameters: 96473596

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : EST:*
1: gb_est1:*
2: gb_est3:*
3: gb_est4:*
4: gb_est5:*
5: gb_est6:*
6: gb_htc:*
7: gb_est2:*
8: gb_est7:*
9: gb_est8:*
10: gb_est9:*
11: gb_gss1:*
12: gb_gss2:*
13: gb_gss3:*
14: gb_gss4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | % Query Match | Length | DB | ID | Description |
|---|---|---|---|---|---|---|
| 1 | 1168.4 | 69.3 | 2712 | 6 | AK054290 | AK054290 Mus muscu |
| 2 | 1168.4 | 69.3 | 3363 | 6 | AK054413 | AK054413 Mus muscu |
| 3 | 962 | 57.1 | 3144 | 6 | AK054301 | AK054301 Mus muscu |
| 4 | 584.4 | 34.7 | 587 | 8 | CV024245 | CV024245 1485 Full |
| 5 | 500.8 | 29.7 | 727 | 2 | BG722442 | BG722442 602693671 |
| 6 | 403.4 | 23.9 | 621 | 9 | DB025815 | DB025815 DB025815 |
| 7 | 364.6 | 21.6 | 4248 | 6 | AK041525 | AK041525 Mus muscu |
| 8 | 364.6 | 21.6 | 4321 | 6 | AK036627 | AK036627 Mus muscu |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| | 9 | 353.8 | 21.0 | 570 | 9 | DB052117 | DB052117 DB052117 |
| | 10 | 353.6 | 21.0 | 2591 | 6 | AK077236 | AK077236 Mus muscu |
| | 11 | 353.4 | 21.0 | 572 | 9 | DB029843 | DB029843 DB029843 |
| c | 12 | 288.2 | 17.1 | 835 | 13 | CW720839 | CW720839 MARC_1130 |
| | 13 | 286.8 | 17.0 | 5439 | 6 | HSM807087 | BX640939 Homo sapi |
| | 14 | 278 | 16.5 | 4315 | 6 | AK087638 | AK087638 Mus muscu |
| | 15 | 276.6 | 16.4 | 703 | 4 | BY720348 | BY720348 BY720348 |
| | 16 | 276.6 | 16.4 | 873 | 8 | CO808332 | CO808332 AGENCOURT |
| | 17 | 275.2 | 16.3 | 675 | 5 | CF913882 | CF913882 B0955G07- |
| c | 18 | 260 | 15.4 | 810 | 13 | CW720841 | CW720841 MARC_1130 |
| | 19 | 238.6 | 14.2 | 375 | 5 | CJ075881 | CJ075881 CJ075881 |
| | 20 | 237.8 | 14.1 | 387 | 9 | DR000137 | DR000137 TC119215 |
| | 21 | 220.2 | 13.1 | 663 | 4 | BY720287 | BY720287 BY720287 |
| | 22 | 220 | 13.0 | 814 | 13 | CW720570 | CW720570 MARC_1129 |
| | 23 | 219.6 | 13.0 | 1020 | 6 | AK136228 | AK136228 Mus muscu |
| | 24 | 215.8 | 12.8 | 735 | 12 | BZ834605 | BZ834605 CH240_209 |
| c | 25 | 214 | 12.7 | 1160 | 5 | CD508522 | CD508522 CDA91-C11 |
| c | 26 | 208 | 12.3 | 627 | 3 | BM942391 | BM942391 UI-M-BH3- |
| | 27 | 201.2 | 11.9 | 2735 | 6 | AK054182 | AK054182 Mus muscu |
| | 28 | 196.4 | 11.6 | 652 | 7 | BB666338 | BB666338 BB666338 |
| | 29 | 189.4 | 11.2 | 623 | 9 | DN424563 | DN424563 LIB4216-1 |
| | 30 | 185.4 | 11.0 | 666 | 7 | BB609187 | BB609187 BB609187 |
| | 31 | 184.6 | 10.9 | 627 | 7 | BB666608 | BB666608 BB666608 |
| | 32 | 179.6 | 10.7 | 611 | 4 | BX489897 | BX489897 DKFZp686N |
| | 33 | 174.2 | 10.3 | 766 | 13 | CW720571 | CW720571 MARC_1129 |
| c | 34 | 173.4 | 10.3 | 531 | 1 | AA224131 | AA224131 zr14e02.r |
| | 35 | 169.8 | 10.1 | 1419 | 10 | DT949269 | DT949269 CFW102-E0 |
| c | 36 | 162.4 | 9.6 | 528 | 3 | BM933826 | BM933826 UI-M-BH3- |
| | 37 | 162.2 | 9.6 | 580 | 2 | BG738138 | BG738138 fp04f05.y |
| | 38 | 157.2 | 9.3 | 936 | 14 | DQ038302 | DQ038302 Pan trogl |
| | 39 | 157 | 9.3 | 642 | 7 | BF058527 | BF058527 7k31h08.x |
| | 40 | 157 | 9.3 | 782 | 7 | AW134052 | AW134052 fi14h07.y |
| | 41 | 157 | 9.3 | 1017 | 14 | DQ038301 | DQ038301 Homo sapi |
| | 42 | 155.6 | 9.2 | 877 | 10 | DT235626 | DT235626 JGI_CAAT8 |
| | 43 | 155.4 | 9.2 | 641 | 7 | AW976636 | AW976636 EST388745 |
| | 44 | 155 | 9.2 | 650 | 5 | CD594261 | CD594261 RK090A3F1 |
| | 45 | 155 | 9.2 | 650 | 5 | CD594319 | CD594319 RK090A4F1 |